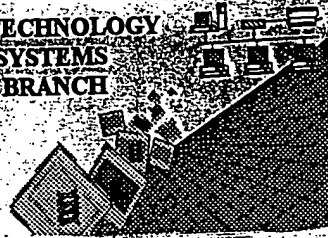BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _____09 | 940,316_____

Source: _____OIPE_____

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PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

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3. Hand Carry directly to:
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
   Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
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Revised 01/29/2002

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/940,316

DATE: 11/20/2002
TIME: 11:24:10

Input Set : D:\30062-20026.txt
Output Set: N:\CRF4\11192002\I940316.raw

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 3 <110> APPLICANT: KOSAN BIOSCIENCES, Inc.
 4       REEVES, CHRISTOPHER
 5       CHU, DANIEL
 6       KHOSLA, CHAITAN
 7       SANTI, DANIEL
 8       WU, KAI
10 <120> TITLE OF INVENTION: POLYKETIDES ENCODING THE fkbA GENE OF THE FK-520 POLYKETIDE
SYNTHASE
11       GENE CLUSTER
13 <130> FILE REFERENCE: 30062-20026.11
15 <140> CURRENT APPLICATION NUMBER: 09/940,316
C--> 16 <141> CURRENT FILING DATE: 2002-11-01
18 <150> PRIOR APPLICATION NUMBER: 09/410,551
19 <151> PRIOR FILING DATE: 1999-10-01
21 <150> PRIOR APPLICATION NUMBER: US 60/139,650
22 <151> PRIOR FILING DATE: 1999-06-17
24 <150> PRIOR APPLICATION NUMBER: US 60/123,810
25 <151> PRIOR FILING DATE: 1999-03-11
27 <150> PRIOR APPLICATION NUMBER: US 60/102,748
28 <151> PRIOR FILING DATE: 1998-10-02
30 <160> NUMBER OF SEQ ID NOS: 72
32 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors

Amino numbering: some digits missing throughout

ERRORED SEQUENCES

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3245 <210> SEQ ID NO: 17
3246 <211> LENGTH: 1488
3247 <212> TYPE: PRT
3248 <213> ORGANISM: Artificial Sequence
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3251 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
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3256  1               5                  10                  15
3258 Ala Ala Val Leu Gly His Val Gly Gly Glu Asp Ile Pro Ala Thr Ala
3259              20                  25                  30
3261 Ala Phe Lys Asp Leu Gly Ile Asp Ser Leu Thr Ala Val Gln Leu Arg
3262          35                  40                  45
3264 Asn Ala Leu Thr Glu Ala Thr Gly Val Arg Leu Asn Ala Thr Ala Val
3265          50                  55                  60
3267 Phe Asp Phe Pro Thr Pro His Val Leu Ala Gly Lys Leu Gly Asp Glu
3268  65                  70                  75                  80
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3420 Thr Val Asp Trp Pro Ala Leu Leu Gly Asp Ala Pro Ala Thr Arg Val
3421              885              890              895
3423 Leu Asp Leu Pro Thr Tyr Ala Phe Gln His Gln Arg Tyr Trp Leu Glu
3424              900              905              910
3426 Ser Ala Arg Pro Ala Ala Ser Asp Ala Gly His Pro Val Leu Gly Ser
3427         915              920              925
3429 Gly Ile Ala Leu Ala Gly Ser Pro Gly Arg Val Phe Thr Gly Ser Val
3430     930              935              940
3432 Pro Thr Gly Ala Asp Arg Ala Val Phe Val Ala Glu Leu Ala Leu Ala
3433 945              950              955              960
3435 Ala Ala Asp Ala Val Asp Cys Ala Thr Val Glu Arg Leu Asp Ile Ala
3436              965              970              975
3438 Ser Val Pro Gly Arg Pro Gly His Gly Arg Thr Thr Val Gln Thr Trp
3439              980              985              990
3441 Val Asp Glu Pro Ala Asp Asp Gly Arg Arg Arg Phe Thr Val His Thr
3442         995              1000              1005
3444 Arg Thr Gly Asp Ala Pro Trp Thr Leu His Ala Glu Gly Val Leu Arg
3445     1010              1015              1020
3447 Pro His Gly Thr Ala Leu Pro Asp Ala Ala Asp Ala Glu Trp Pro Pro
3448 1025              1030              1035              104
3450 Pro Gly Ala Val Pro Ala Asp Gly Leu Pro Gly Val Trp Arg Arg Gly
3451              1045              1050              1055
3453 Asp Gln Val Phe Ala Glu Ala Glu Val Asp Gly Pro Asp Gly Phe Val
3454         1060              1065              1070
3456 Val His Pro Asp Leu Leu Asp Ala Val Phe Ser Ala Val Gly Asp Gly
3457     1075              1080              1085
3459 Ser Arg Gln Pro Ala Gly Trp Arg Asp Leu Thr Val His Ala Ser Asp
3460 1090              1095              1100
3462 Ala Thr Val Leu Arg Ala Cys Leu Thr Arg Arg Thr Asp Gly Ala Met
3463 1105              1110              1115              112
3465 Gly Phe Ala Ala Phe Asp Gly Ala Gly Leu Pro Val Leu Thr Ala Glu
3466              1125              1130              1135
3468 Ala Val Thr Leu Arg Glu Val Ala Ser Pro Ser Gly Ser Glu Glu Ser
3469              1140              1145              1150
3471 Asp Gly Leu His Arg Leu Glu Trp Leu Ala Val Ala Glu Ala Val Tyr
3472         1155              1160              1165
3474 Asp Gly Asp Leu Pro Glu Gly His Val Leu Ile Thr Ala Ala His Pro
3475     1170              1175              1180
3477 Asp Asp Pro Glu Asp Ile Pro Thr Arg Ala His Thr Arg Ala Thr Arg
3478 1185              1190              1195              120
3480 Val Leu Thr Ala Leu Gln His His Leu Thr Thr Thr Asp His Thr Leu
3481              1205              1210              1215
3483 Ile Val His Thr Thr Thr Asp Pro Ala Gly Ala Thr Val Thr Gly Leu
3484              1220              1225              1230
3486 Thr Arg Thr Ala Gln Asn Glu His Pro His Arg Ile Arg Leu Ile Glu
3487         1235              1240              1245
3489 Thr Asp His Pro His Thr Pro Leu Pro Leu Ala Gln Leu Ala Thr Leu
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RAW SEQUENCE LISTING   DATE: 11/20/2002
PATENT APPLICATION: US/09/940,316   TIME: 11:24:10

Input Set : D:\30062-20026.txt
Output Set: N:\CRF4\11192002\I940316.raw

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3490    1250              1255              1260
3492 Asp His Pro His Leu Arg Leu Thr His His Thr Leu His His Pro His
E--> 3493 265            1270              1275              128
3495 Leu Thr Pro Leu His Thr Thr Thr Pro Pro Thr Thr Thr Pro Leu Asn
3496              1285          1290              1295
3498 Pro Glu His Ala Ile Ile Ile Thr Gly Gly Ser Gly Thr Leu Ala Gly
3499          1300              1305              1310
3501 Ile Leu Ala Arg His Leu Asn His Pro His Thr Tyr Leu Leu Ser Arg
3502      1315              1320              1325
3504 Thr Pro Pro Pro Asp Ala Thr Pro Gly Thr His Leu Pro Cys Asp Val
3505    1330              1335              1340
3507 Gly Asp Pro His Gln Leu Ala Thr Thr Leu Thr His Ile Pro Gln Pro
E--> 3508 345            1350              1355              136
3510 Leu Thr Ala Ile Phe His Thr Ala Ala Thr Leu Asp Asp Gly Ile Leu
3511              1365          1370              1375
3513 His Ala Leu Thr Pro Asp Arg Leu Thr Thr Val Leu His Pro Lys Ala
3514            1380              1385              1390
3516 Asn Ala Ala Trp His Leu His His Leu Thr Gln Asn Gln Pro Leu Thr
3517          1395              1400              1405
3519 His Phe Val Leu Tyr Ser Ser Ala Ala Ala Val Leu Gly Ser Pro Gly
3520    1410              1415              1420
3522 Gln Gly Asn Tyr Ala Ala Ala Asn Ala Phe Leu Asp Ala Leu Ala Thr
E--> 3523 425            1430              1435              144
3525 His Arg His Thr Leu Gly Gln Pro Ala Thr Ser Ile Ala Trp Gly Met
3526            1445              1450              1455
3528 Trp His Thr Thr Ser Thr Leu Thr Gly Gln Leu Asp Asp Ala Asp Arg
3529          1460              1465              1470
3531 Asp Arg Ile Arg Arg Gly Gly Phe Leu Pro Ile Thr Asp Asp Glu Gly
3532      1475              1480              1485
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3933 <211> LENGTH: 1517
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3938 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
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3946            20              25              30
3948 Lys Asp Leu Gly Ile Asp Ser Leu Thr Ala Val Gln Leu Arg Asn Ala
3949          35              40              45
3951 Leu Thr Glu Ala Thr Gly Val Arg Leu Asn Ala Thr Ala Val Phe Asp
3952      50              55              60
3954 Phe Pro Thr Pro His Val Leu Ala Gly Lys Leu Gly Asp Glu Leu Thr
3955 65              70              75              80
3957 Gly Thr Arg Ala Pro Val Val Pro Arg Thr Ala Ala Thr Ala Gly Ala
3958            85              90              95
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4107 Asp Val Val Thr Val Ala Thr Leu Arg Arg Asp Asp Gly Asp Ala Thr
4108               885                 890             Val His Gly Val Thr Val
                                                                          895
4110 Arg Met Leu Thr Ala Leu Ala Gln Ala Tyr Val His Gly Val Thr Val
4111               900                   905             910
4113 Asp Trp Pro Ala Ile Leu Gly Thr Thr Thr Thr Arg Val Leu Asp Leu
4114           915                 920                 925
4116 Pro Thr Tyr Ala Phe Gln His Gln Arg Tyr Trp Leu Glu Ser Ala Arg
4117     930                 935                     940
4119 Pro Ala Ala Ser Asp Ala Gly His Pro Val Leu Gly Ser Gly Ile Ala
4120 945                 950                 955                 960
4122 Leu Ala Gly Ser Pro Gly Arg Val Phe Thr Gly Ser Val Pro Thr Gly
4123               965                 970                 975
4125 Ala Asp Arg Ala Val Phe Val Ala Glu Leu Ala Leu Ala Ala Ala Asp
4126           980                 985                 990
4128 Ala Val Asp Cys Ala Thr Val Glu Arg Leu Asp Ile Ala Ser Val Pro
4129           995                 1000                1005
4131 Gly Arg Pro Gly His Gly Arg Thr Thr Val Gln Thr Trp Val Asp Glu
4132     1010                 1015                1020
4134 Pro Ala Asp Asp Gly Arg Arg Arg Phe Thr Val His Thr Arg Thr Gly
E--> 4135 025                1030                1035                1040
4137 Asp Ala Pro Trp Thr Leu His Ala Glu Gly Val Leu Arg Pro His Gly
4138               1045                1050                1055
4140 Thr Ala Leu Pro Asp Ala Ala Asp Ala Glu Trp Pro Pro Pro Gly Ala
4141           1060                1065                1070
4143 Val Pro Ala Asp Gly Leu Pro Gly Val Trp Arg Arg Gly Asp Gln Val
4144     1075                1080                1085
4146 Phe Ala Glu Ala Glu Val Asp Gly Pro Asp Gly Phe Val Val His Pro
4147     1090                1095                1100
4149 Asp Leu Leu Asp Ala Val Phe Ser Ala Val Gly Asp Gly Ser Arg Gln
E--> 4150 105                1110                1115                1120
4152 Pro Ala Gly Trp Arg Asp Leu Thr Val His Ala Ser Asp Ala Thr Val
4153               1125                1130                1135
4155 Leu Arg Ala Cys Leu Thr Arg Arg Thr Asp Gly Ala Met Gly Phe Ala
4156           1140                1145                1150
4158 Ala Phe Asp Gly Ala Gly Leu Pro Val Leu Thr Ala Glu Ala Val Thr
4159     1155                1160                1165
4161 Leu Arg Glu Val Ala Ser Pro Ser Gly Ser Glu Glu Ser Asp Gly Leu
4162     1170                1175                1180
4164 His Arg Leu Glu Trp Leu Ala Val Ala Glu Ala Val Tyr Asp Gly Asp
E--> 4165 185                1190                1195                1200
4167 Leu Pro Glu Gly His Val Leu Ile Thr Ala Ala His Pro Asp Asp Pro
4168               1205                1210                1215
4170 Glu Asp Ile Pro Thr Arg Ala His Thr Arg Ala Thr Arg Val Leu Thr
4171     1220                1225                1230
4173 Ala Leu Gln His His Leu Thr Thr Thr Asp His Thr Leu Ile Val His
4174     1235                1240                1245
4176 Thr Thr Thr Asp Pro Ala Gly Ala Thr Val Thr Gly Leu Thr Arg Thr
4177  1250                1255                1260
4179 Ala Gln Asn Glu His Pro His Arg Ile Arg Leu Ile Glu Thr Asp His
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E--> 4180 265               1270               1275               1280
     4182 Pro His Thr Pro Leu Pro Leu Ala Gln Leu Ala Thr Leu Asp His Pro
     4183          1285              1290               1295
     4185 His Leu Arg Leu Thr His His Thr Leu His His Pro His Leu Thr Pro
     4186          1300              1305 -             1310
     4188 Leu His Thr Thr Thr Pro Pro Thr Thr Thr Pro Leu Asn Pro Glu His
     4189     1315              1320              1325
     4191 Ala Ile Ile Ile Thr Gly Gly Ser Gly Thr Leu Ala Gly Ile Leu Ala
     4192     1330              1335              1340
     4194 Arg His Leu Asn His Pro His Thr Tyr Leu Leu Ser Arg Thr Pro Pro
E--> 4195 345               1350               1355               1360
     4197 Pro Asp Ala Thr Pro Gly Thr His Leu Pro Cys Asp Val Gly Asp Pro
     4198          1365              1370               1375
     4200 His Gln Leu Ala Thr Thr Leu Thr His Ile Pro Gln Pro Leu Thr Ala
     4201          1380              1385              1390
     4203 Ile Phe His Thr Ala Ala Thr Leu Asp Asp Gly Ile Leu His Ala Leu
     4204     1395              1400              1405
     4206 Thr Pro Asp Arg Leu Thr Thr Val Leu His Pro Lys Ala Asn Ala Ala
     4207     1410              1415              1420
     4209 Trp His Leu His His Leu Thr Gln Asn Gln Pro Leu Thr His Phe Val
E--> 4210 425               1430               1435               1440
     4212 Leu Tyr Ser Ser Ala Ala Ala Val Leu Gly Ser Pro Gly Gln Gly Asn
     4213               1445              1450              1455
     4215 Tyr Ala Ala Ala Asn Ala Phe Leu Asp Ala Leu Ala Thr His Arg His
     4216          1460              1465              1470
     4218 Thr Leu Gly Gln Pro Ala Thr Ser Ile Ala Trp Gly Met Trp His Thr
     4219          1475              1480              1485
     4221 Thr Ser Thr Leu Thr Gly Gln Leu Asp Asp Ala Asp Arg Asp Arg Ile
     4222     1490              1495              1500
     4224 Arg Arg Gly Gly Phe Leu Pro Ile Thr Asp Asp Glu Gly
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     4618 <213> ORGANISM: Artificial Sequence
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     4628 Val Leu Gly His Val Gly Gly Glu Asp Ile Pro Ala Thr Ala Ala Phe
     4629             20                25                30
     4631 Lys Asp Leu Gly Ile Asp Ser Leu Thr Ala Val Gln Leu Arg Asn Ala
     4632          35                40                45
     4634 Leu Thr Glu Ala Thr Gly Val Arg Leu Asn Ala Thr Ala Val Phe Asp
     4635     50                55                60
     4637 Phe Pro Thr Pro His Val Leu Ala Gly Lys Leu Gly Asp Glu Leu Thr
     4638  65                70                75                80
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       4787 Ala Leu Ala His Leu Tyr Val Asn Gly Val Thr Val Asp Trp Pro Ala
       4788 865               870             875             880
       4790 Leu Leu Gly Asp Ala Pro Ala Thr Arg Val Leu Asp Leu Pro Thr Tyr
       4791               885             890               -895
       4793 Ala Phe Gln His Gln Arg Tyr Trp Leu Glu Ser Ala Arg Pro Ala Ala
       4794               900             905             910
       4796 Ser Asp Ala Gly His Pro Val Leu Gly Ser Gly Ile Ala Leu Ala Gly
       4797       915               920             925
       4799 Ser Pro Gly Arg Val Phe Thr Gly Ser Val Pro Thr Gly Ala Asp Arg
       4800   930             935                 940
       4802 Ala Val Phe Val Ala Glu Leu Ala Leu Ala Ala Ala Asp Ala Val Asp
       4803 945             950             955                 960
       4805 Cys Ala Thr Val Glu Arg Leu Asp Ile Ala Ser Val Pro Gly Arg Pro
       4806             965             970               975
       4808 Gly His Gly Arg Thr Thr Val Gln Thr Trp Val Asp Glu Pro Ala Asp
       4809         980             985             990
       4811 Asp Gly Arg Arg Arg Phe Thr Val His Thr Arg Thr Gly Asp Ala Pro
       4812       995             1000            1005
       4814 Trp Thr Leu His Ala Glu Gly Val Leu Arg Pro His Gly Thr Ala Leu
       4815     1010            1015              1020
       4817 Pro Asp Ala Ala Asp Ala Glu Trp Pro Pro Pro Gly Ala Val Pro Ala
E-->   4818 025             1030            1035            1040
       4820 Asp Gly Leu Pro Gly Val Trp Arg Arg Gly Asp Gln Val Phe Ala Glu
       4821             1045            1050            1055
       4823 Ala Glu Val Asp Gly Pro Asp Gly Phe Val Val His Pro Asp Leu Leu
       4824         1060            1065          1070
       4826 Asp Ala Val Phe Ser Ala Val Gly Asp Gly Ser Arg Gln Pro Ala Gly
       4827     1075            1080            1085
       4829 Trp Arg Asp Leu Thr Val His Ala Ser Asp Ala Thr Val Leu Arg Ala
       4830     1090            1095            1100
       4832 Cys Leu Thr Arg Arg Thr Asp Gly Ala Met Gly Phe Ala Ala Phe Asp
E-->   4833 105             1110            1115            1120
       4835 Gly Ala Gly Leu Pro Val Leu Thr Ala Glu Ala Val Thr Leu Arg Glu
       4836             1125            1130            1135
       4838 Val Ala Ser Pro Ser Gly Ser Glu Glu Ser Asp Gly Leu His Arg Leu
       4839         1140            1145            1150
       4841 Glu Trp Leu Ala Val Ala Glu Ala Val Tyr Asp Gly Asp Leu Pro Glu
       4842     1155            1160            1165
       4844 Gly His Val Leu Ile Thr Ala Ala His Pro Asp Asp Pro Glu Asp Ile
       4845     1170            1175            1180
       4847 Pro Thr Arg Ala His Thr Arg Ala Thr Arg Val Leu Thr Ala Leu Gln
E-->   4848 185             1190            1195            1200
       4850 His His Leu Thr Thr Thr Asp His Thr Leu Ile Val His Thr Thr Thr
       4851             1205            1210            1215
       4853 Asp Pro Ala Gly Ala Thr Val Thr Gly Leu Thr Arg Thr Ala Gln Asn
       4854             1220            1225            1230
       4856 Glu His Pro His Arg Ile Arg Leu Ile Glu Thr Asp His Pro His Thr
       4857         1235            1240            1245
       4859 Pro Leu Pro Leu Ala Gln Leu Ala Thr Leu Asp His Pro His Leu Arg
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4860    1250                1255                1260
4862 Leu Thr His His Thr Leu His His Pro His Leu Thr Pro Leu His Thr
E--> 4863 265         .        1270            1275            1280
4865 Thr Thr Pro Pro Thr Thr Thr Pro Leu Asn Pro Glu His Ala Ile Ile
4866                1285        .        1290            1295
4868 Ile Thr Gly Gly Ser Gly Thr Leu Ala Gly Ile Leu Ala Arg His Leu
4869         .      1300      .         1305      .         1310
4871 Asn His Pro His Thr Tyr Leu Leu Ser Arg Thr Pro Pro Pro Asp Ala
4872        1315                1320              1325
4874 Thr Pro Gly Thr His Leu Pro Cys Asp Val Gly Asp Pro His Gln Leu
4875    1330  .             1335              1340
4877 Ala Thr Thr Leu Thr His Ile Pro Gln Pro Leu Thr Ala Ile Phe His
E--> 4878 345          1350            1355  ..          1360
4880 Thr Ala Ala Thr Leu Asp Asp Gly Ile Leu His Ala Leu Thr Pro Asp
.    4881        .      1365            1370    .  .      1375
4883 Arg Leu Thr Thr Val Leu His Pro Lys Ala Asn Ala Ala Trp His Leu
4884            1380      .         1385            1390
4886 His His Leu Thr Gln Asn Gln Pro Leu Thr His Phe Val Leu Tyr Ser
4887        1395            1400    ..          1405
4889 Ser Ala Ala Ala Val Leu Gly Ser Pro Gly Gln Gly Asn Tyr Ala Ala
4890    1410      ..          1415            1420
4892 Ala Asn Ala Phe Leu Asp Ala Leu Ala Thr His Arg His Thr Leu Gly
E--> 4893 425          1430      :         1435            1440
4895 Gln Pro Ala Thr Ser Ile Ala Trp Gly Met Trp His Thr Thr Ser Thr
4896            .  . 1445            1450 .  .          1455
4898 Leu Thr Gly Gln Leu Asp Asp Ala Asp Arg Asp Arg Ile Arg Arg Gly
4899            1460      .         1465            1470
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4902        1475            1480  .
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5301 <211> LENGTH: 1509 ·
5302 <212> TYPE: PRT
5303 <213> ORGANISM: Artificial Sequence
5305 <220> FEATURE:
5306 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
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5309 <400> SEQUENCE: 23
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5313 Val Leu Gly His Val Gly Gly Glu Asp Ile Pro Ala Thr Ala Ala Phe
5314            20              25              30
5316 Lys Asp Leu Gly Ile Asp Ser Leu Thr Ala Val Gln Leu Arg Asn Ala
5317        35              40              45
5319 Leu Thr Glu Ala Thr Gly Val Arg Leu Asn Ala Thr Ala Val Phe Asp
5320    50              55              60
5322 Phe Pro Thr Pro His Val Leu Ala Gly Lys Leu Gly Asp Glu Leu Thr
5323 65              70              75              80
5325 Gly Thr Arg Ala Pro Val Val Pro Arg Thr Ala Ala Thr Ala Gly Ala
5326            85              90              95
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     5475 Arg Arg Asp Asp Gly Asp Ala Thr Arg Met Leu Thr Ala Leu Ala Gln
     5476           885             890                -        895
     5478 Ala Tyr Val His Gly Val Thr Val Asp Trp Pro Ala Ile Leu Gly Thr
     5479       900             905                 910
     5481 Thr Thr Thr Arg Val Leu Asp Leu Pro Thr Tyr Ala Phe Gln His Gln
     5482        915             920              925
     5484 Arg Tyr Trp Leu Glu Ser Ala Arg Pro Ala Ala Ser Asp Ala Gly His
     5485     930             935             940
     5487 Pro Val Leu Gly Ser Gly Ile Ala Leu Ala Gly Ser Pro Gly Arg Val
     5488 945             950             955                 960
     5490 Phe Thr Gly Ser Val Pro Thr Gly Ala Asp Arg Ala Val Phe Val Ala
     5491              965             970             975
     5493 Glu Leu Ala Leu Ala Ala Ala Asp Ala Val Asp Cys Ala Thr Val Glu
     5494           980             985                 990
     5496 Arg Leu Asp Ile Ala Ser Val Pro Gly Arg Pro Gly His Gly Arg Thr
     5497      995             1000              1005
     5499 Thr Val Gln Thr Trp Val Asp Glu Pro Ala Asp Asp Gly Arg Arg Arg
     5500     1010             1015             1020
     5502 Phe Thr Val His Thr Arg Thr Gly Asp Ala Pro Trp Thr Leu His Ala
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     5505 Glu Gly Val Leu Arg Pro His Gly Thr Ala Leu Pro Asp Ala Ala Asp
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     5509         1060             1065             1070
     5511 Val Trp Arg Arg Gly Asp Gln Val Phe Ala Glu Ala Glu Val Asp Gly
     5512     1075             1080             1085
     5514 Pro Asp Gly Phe Val Val His Pro Asp Leu Leu Asp Ala Val Phe Ser
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     5523 Thr Asp Gly Ala Met Gly Phe Ala Ala Phe Asp Gly Ala Gly Leu Pro
     5524         1140             1145             1150
     5526 Val Leu Thr Ala Glu Ala Val Thr Leu Arg Glu Val Ala Ser Pro Ser
     5527     1155             1160             1165
     5529 Gly Ser Glu Glu Ser Asp Gly Leu His Arg Leu Glu Trp Leu Ala Val
     5530 1170             1175             1180
     5532 Ala Glu Ala Val Tyr Asp Gly Asp Leu Pro Glu Gly His Val Leu Ile
E--> 5533 185             1190             1195             1200
     5535 Thr Ala Ala His Pro Asp Asp Pro Glu Asp Ile Pro Thr Arg Ala His
     5536             1205             1210             1215
     5538 Thr Arg Ala Thr Arg Val Leu Thr Ala Leu Gln His His Leu Thr Thr
     5539         1220             1225             1230
     5541 Thr Asp His Thr Leu Ile Val His Thr Thr Asp Pro Ala Gly Ala
     5542     1235             1240             1245
     5544 Thr Val Thr Gly Leu Thr Arg Thr Ala Gln Asn Glu His Pro His Arg
     5545 1250             1255             1260
     5547 Ile Arg Leu Ile Glu Thr Asp His Pro His Thr Pro Leu Pro Leu Ala
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/940,316

Input Set : D:\30062-20026.txt
Output Set: N:\CRF4\11192002\I940316.raw

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E--> 5548 265               1270            1275              1280
     5550 Gln Leu Ala Thr Leu Asp His Pro His Leu Arg Leu Thr His His Thr
     5551               1285            1290              1295
     5553 Leu His His Pro His Leu Thr Pro Leu His Thr Thr Thr Pro Pro Thr
     5554          1300              1305              1310
     5556 Thr Thr Pro Leu Asn Pro Glu His Ala Ile Ile Ile Thr Gly Gly Ser
     5557      1315              1320              1325
     5559 Gly Thr Leu Ala Gly Ile Leu Ala Arg His Leu Asn His Pro His Thr
     5560     1330              1335              1340
     5562 Tyr Leu Leu Ser Arg Thr Pro Pro Pro Asp Ala Thr Pro Gly Thr His
E--> 5563 345               1350            1355              1360
     5565 Leu Pro Cys Asp Val Gly Asp Pro His Gln Leu Ala Thr Thr Leu Thr
     5566          1365              1370              1375
     5568 His Ile Pro Gln Pro Leu Thr Ala Ile Phe His Thr Ala Ala Thr Leu
     5569          1380              1385              1390
     5571 Asp Asp Gly Ile Leu His Ala Leu Thr Pro Asp Arg Leu Thr Thr Val
     5572      1395              1400              1405
     5574 Leu His Pro Lys Ala Asn Ala Ala Trp His Leu His His Leu Thr Gln
     5575     1410              1415              1420
     5577 Asn Gln Pro Leu Thr His Phe Val Leu Tyr Ser Ser Ala Ala Ala Val
E--> 5578 425               1430            1435              1440
     5580 Leu Gly Ser Pro Gly Gln Gly Asn Tyr Ala Ala Ala Asn Ala Phe Leu
     5581               1445            1450              1455
     5583 Asp Ala Leu Ala Thr His Arg His Thr Leu Gly Gln Pro Ala Thr Ser
     5584          1460              1465              1470
     5586 Ile Ala Trp Gly Met Trp His Thr Thr Ser Thr Leu Thr Gly Gln Leu
     5587          1475              1480              1485
     5589 Asp Asp Ala Asp Arg Asp Arg Ile Arg Arg Gly Gly Phe Leu Pro Ile
     5590     1490              1495              1500
     5592 Thr Asp Asp Glu Gly
E--> 5593 505
     6007 <210> SEQ ID NO: 25
     6008 <211> LENGTH: 1574
     6009 <212> TYPE: PRT
     6010 <213> ORGANISM: Artificial Sequence
     6012 <220> FEATURE:
     6013 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
     6014      synthase fragment
     6016 <400> SEQUENCE: 25
     6017 Met Arg Leu Tyr Glu Ala Ala Arg Arg Thr Gly Ser Pro Val Val Val
     6018   1           5                   10                15
     6020 Ala Ala Ala Leu Asp Asp Ala Pro Asp Val Pro Leu Leu Arg Gly Leu
     6021           20                  25                  30
     6023 Arg Arg Thr Thr Val Arg Arg Ala Ala Val Arg Glu Arg Ser Leu Ala
     6024           35                  40                  45
     6026 Asp Arg Ser Pro Cys Cys Pro Thr Thr Ser Ala Pro Thr Pro Pro Ser
     6027      50                  55                  60
     6029 Arg Ser Ser Trp Asn Ser Thr Ala Thr Val Leu Gly His Leu Gly Ala
     6030 65                  70                  75              80
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6179 Leu Ala Thr Thr Arg Glu Leu Arg Tyr Asp Arg Pro His Thr Ala Ile
6180 865            870            875            880
6182 Pro Asn Asp Pro Thr Thr Ala Glu Tyr Trp Ala Glu Gln Val Arg Asn
6183            885            890            895
6185 Pro Val Leu Phe His Ala His Thr Gln Arg Tyr Pro Asp Ala Val Phe
6186            900            905            910
6188 Val Glu Ile Gly Pro Gly Gln Asp Leu Ser Pro Leu Val Asp Gly Ile
6189            915            920            925
6191 Ala Leu Gln Asn Gly Thr Ala Asp Glu Val His Ala Leu His Thr Ala
6192            930            935            940
6194 Leu Ala Arg Leu Phe Thr Arg Gly Ala Thr Leu Asp Trp Ser Arg Ile
6195 945            950            955            960
6197 Leu Gly Gly Ala Ser Arg His Asp Pro Asp Val Pro Ser Tyr Ala Phe
6198            965            970            975
6200 Gln Arg Arg Pro Tyr Trp Ile Glu Ser Ala Pro Pro Ala Thr Ala Asp
6201            980            985            990
6203 Ser Gly His Pro Val Leu Gly Thr Gly Val Ala Val Ala Gly Ser Pro
6204            995            1000            1005
6206 Gly Arg Val Phe Thr Gly Pro Val Pro Ala Gly Ala Asp Arg Ala Val
6207 1010            1015            1020
6209 Phe Ile Ala Glu Leu Ala Leu Ala Ala Ala Asp Ala Thr Asp Cys Ala
E--> 6210 025            1030            1035            104
6212 Thr Val Glu Gln Leu Asp Val Thr Ser Val Pro Gly Gly Ser Ala Arg
6213            1045            1050            1055
6215 Gly Arg Ala Thr Ala Gln Thr Trp Val Asp Glu Pro Ala Ala Asp Gly
6216            1060            1065            1070
6218 Arg Arg Arg Phe Thr Val His Thr Arg Val Gly Asp Ala Pro Trp Thr
6219            1075            1080            1085
6221 Leu His Ala Glu Gly Val Leu Arg Pro Gly Arg Val Pro Gln Pro Glu
6222 1090            1095            1100
6224 Ala Val Asp Thr Ala Trp Pro Pro Pro Gly Ala Val Pro Ala Asp Gly
E--> 6225 105            1110            1115            112
6227 Leu Pro Gly Ala Trp Arg Arg Ala Asp Gln Val Phe Val Glu Ala Glu
6228            1125            1130            1135
6230 Val Asp Ser Pro Asp Gly Phe Val Ala His Pro Asp Leu Leu Asp Ala
6231            1140            1145            1150
6233 Val Phe Ser Ala Val Gly Asp Gly Ser Arg Gln Pro Thr Gly Trp Arg
6234            1155            1160            1165
6236 Asp Leu Ala Val His Ala Ser Asp Ala Thr Val Leu Arg Ala Cys Leu
6237 1170            1175            1180
6239 Thr Arg Arg Asp Ser Gly Val Val Glu Leu Ala Ala Phe Asp Gly Ala
E--> 6240 185            1190            1195            120
6242 Gly Met Pro Val Leu Thr Ala Glu Ser Val Thr Leu Gly Glu Val Ala
6243            1205            1210            1215
6245 Ser Ala Gly Gly Ser Asp Glu Ser Asp Gly Leu Leu Arg Leu Glu Trp
6246            1220            1225            1230
6248 Leu Pro Val Ala Glu Ala His Tyr Asp Gly Ala Asp Glu Leu Pro Glu
6249            1235            1240            1245
6251 Gly Tyr Thr Leu Ile Thr Ala Thr His Pro Asp Asp Pro Asp Asp Pro
```

```
      6252    1250                 1255                 1260
      6254 Thr Asn Pro His Asn Thr Pro Thr Arg Thr His Thr Gln Thr Thr Arg
E-->  6255 265                 1270                 1275                 128
      6257 Val Leu Thr Ala Leu Gln His His Leu Ile Thr Thr Asn His Thr Leu
      6258                 1285                 1290                 1295
      6260 Ile Val His Thr Thr Thr Asp Pro Pro Gly Ala Ala Val Thr Gly Leu
      6261                 1300                 1305                 1310
      6263 Thr Arg Thr Ala Gln Asn Glu His Pro Gly Arg Ile His Leu Ile Glu
      6264            1315                 1320                 1325
      6266 Thr His His Pro His Thr Pro Leu Pro Leu Thr Gln Leu Thr Thr Leu
      6267    1330                 1335                 1340
      6269 His Gln Pro His Leu Arg Leu Thr Asn Asn Thr Leu His Thr Pro His
E-->  6270 345                 1350                 1355                 136
      6272 Leu Thr Pro Ile Thr Thr His His Asn Thr Thr Thr Thr Thr Pro Asn
      6273                 1365                 1370                 1375
      6275 Thr Pro Pro Leu Asn Pro Asn His Ala Ile Leu Ile Thr Gly Gly Ser
      6276                 1380                 1385                 1390
      6278 Gly Thr Leu Ala Gly Ile Leu Ala Arg His Leu Asn His Pro His Thr
      6279            1395                 1400                 1405
      6281 Tyr Leu Leu Ser Arg Thr Pro Pro Pro Thr Thr Pro Gly Thr His
      6282    1410                 1415                 1420
      6284 Ile Pro Cys Asp Leu Thr Asp Pro Thr Gln Ile Thr Gln Ala Leu Thr
E-->  6285 425                 1430                 1435                 144
      6287 His Ile Pro Gln Pro Leu Thr Gly Ile Phe His Thr Ala Ala Thr Leu
      6288                 1445                 1450                 1455
      6290 Asp Asp Ala Thr Leu Thr Asn Leu Thr Pro Gln His Leu Thr Thr Thr
      6291            1460                 1465                 1470
      6293 Leu Gln Pro Lys Ala Asp Ala Ala Trp His Leu His His His Thr Gln
      6294            1475                 1480                 1485
      6296 Asn Gln Pro Leu Thr His Phe Val Leu Tyr Ser Ser Ala Ala Ala Thr
      6297    1490                 1495                 1500
      6299 Leu Gly Ser Pro Gly Gln Ala Asn Tyr Ala Ala Ala Asn Ala Phe Leu
E-->  6300 505                 1510                 1515                 152
      6302 Asp Ala Leu Ala Thr His Arg His Thr Gln Gly Gln Pro Ala Thr Thr
      6303                 1525                 1530                 1535
      6305 Ile Ala Trp Gly Met Trp His Thr Thr Thr Thr Leu Thr Ser Gln Leu
      6306            1540                 1545                 1550
      6308 Thr Asp Ser Asp Arg Asp Arg Ile Arg Arg Gly Gly Phe Leu Pro Ile
      6309            1555                 1560                 1565
      6311 Ser Asp Asp Glu Gly Met
      6312    1570
      6722 <210> SEQ ID NO: 27
      6723 <211> LENGTH: 1557
      6724 <212> TYPE: PRT
      6725 <213> ORGANISM: Artificial Sequence
      6727 <220> FEATURE:
      6728 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
      6729         synthase fragment
      6731 <400> SEQUENCE: 27
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      6879 Glu Ala Arg Ala Val Leu Gly Glu Gly Val Glu Ile Ala Ala Val Asn
      6880 785                 790                 795                 800
      6882 Gly Pro Ser Ser Val Val Leu Ser Gly Asp Glu Ala Ala Val Leu Gln
      6883                     805                 810                 815
      6885 Ala Ala Glu Gly Leu Gly Lys Trp Thr Arg Leu Ala Thr Ser His Ala
      6886             820                 825                 830
      6888 Phe His Ser Ala Arg Met Glu Pro Met Leu Glu Glu Phe Arg Ala Val
      6889             835                 840                 845
      6891 Ala Glu Gly Leu Thr Tyr Arg Thr Pro Gln Val Ser Met Ala Val Gly
      6892     850                 855                 860
      6894 Asp Gln Val Thr Thr Ala Glu Tyr Trp Val Arg Gln Val Arg Asp Thr
      6895 865                 870                 875                 880
      6897 Val Arg Phe Gly Glu Gln Val Ala Ser Tyr Glu Asp Ala Val Phe Val
      6898                 885                 890                 895
      6900 Glu Leu Gly Ala Asp Arg Ser Leu Ala Arg Leu Val Asp Gly Val Ala
      6901             900                 905                 910
      6903 Met Leu His Gly Asp His Glu Ile Gln Ala Ala Ile Gly Ala Leu Ala
      6904             915                 920                 925
      6906 His Leu Tyr Val Asn Gly Val Thr Val Asp Trp Pro Ala Leu Leu Gly
      6907     930                 935                 940
      6909 Asp Ala Pro Ala Thr Arg Val Leu Asp Leu Pro Thr Tyr Ala Phe Gln
      6910 945                 950                 955                 960
      6912 His Gln Arg Tyr Trp Leu Glu Ser Ala Pro Pro Ala Thr Ala Asp Ser
      6913                 965                 970                 975
      6915 Gly His Pro Val Leu Gly Thr Gly Val Ala Val Ala Gly Ser Pro Gly
      6916             980                 985                 990
      6918 Arg Val Phe Thr Gly Pro Val Pro Ala Gly Ala Asp Arg Ala Val Phe
      6919             995                 1000                1005
      6921 Ile Ala Glu Leu Ala Leu Ala Ala Ala Asp Ala Thr Asp Cys Ala Thr
      6922     1010                1015                1020
      6924 Val Glu Gln Leu Asp Val Thr Ser Val Pro Gly Gly Ser Ala Arg Gly
E-->  6925 025                 1030                1035                104
      6927 Arg Ala Thr Ala Gln Thr Trp Val Asp Glu Pro Ala Ala Asp Gly Arg
      6928                 1045                1050                1055
      6930 Arg Arg Phe Thr Val His Thr Arg Val Gly Asp Ala Pro Trp Thr Leu
      6931             1060                1065                1070
      6933 His Ala Glu Gly Val Leu Arg Pro Gly Arg Val Pro Gln Pro Glu Ala
      6934         1075                1080                1085
      6936 Val Asp Thr Ala Trp Pro Pro Pro Gly Ala Val Pro Ala Asp Gly Leu
      6937     1090                1095                1100
      6939 Pro Gly Ala Trp Arg Arg Ala Asp Gln Val Phe Val Glu Ala Glu Val
E-->  6940 105                 1110                1115                112
      6942 Asp Ser Pro Asp Gly Phe Val Ala His Pro Asp Leu Leu Asp Ala Val
      6943                 1125                1130                1135
      6945 Phe Ser Ala Val Gly Asp Gly Ser Arg Gln Pro Thr Gly Trp Arg Asp
      6946             1140                1145                1150
      6948 Leu Ala Val His Ala Ser Asp Ala Thr Val Leu Arg Ala Cys Leu Thr
      6949         1155                1160                1165
      6951 Arg Arg Asp Ser Gly Val Val Glu Leu Ala Ala Phe Asp Gly Ala Gly
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        6952   1170                1175                1180
        6954 Met Pro Val Leu Thr Ala Glu Ser Val Thr Leu Gly Glu Val Ala Ser
E--> 6955 185                1190                1195                120
        6957 Ala Gly Gly Ser Asp Glu Ser Asp Gly Leu Leu Arg Leu Glu Trp Leu
        6958'              1205                1210                1215
        6960 Pro Val Ala Glu Ala His Tyr Asp Gly Ala Asp Glu Leu Pro Glu Gly
        6961              1220                1225                1230
        6963 Tyr Thr Leu Ile Thr Ala Thr His Pro Asp Asp Pro Asp Asp Pro Thr
        6964           1235                1240                1245
        6966 Asn Pro His Asn Thr Pro Thr Arg Thr His Thr Gln Thr Thr Arg Val
        6967   1250                1255                1260
        6969 Leu Thr Ala Leu Gln His His Leu Ile Thr Thr Asn His Thr Leu Ile
E--> 6970 265                1270                1275                128
        6972 Val His Thr Thr Thr Asp Pro Pro Gly Ala Ala Val Thr Gly Leu Thr
        6973              1285                1290                1295
        6975 Arg Thr Ala Gln Asn Glu His Pro Gly Arg Ile His Leu Ile Glu Thr
        6976              1300                1305                1310
        6978 His His Pro His Thr Pro Leu Pro Leu Thr Gln Leu Thr Thr Leu His
        6979           1315                1320                1325
        6981 Gln Pro His Leu Arg Leu Thr Asn Asn Thr Leu His Thr Pro His Leu
        6982   1330                1335                1340
        6984 Thr Pro Ile Thr Thr His His Asn Thr Thr Thr Thr Thr Pro Asn Thr
E--> 6985 345                1350                1355                136
        6987 Pro Pro Leu Asn Pro Asn His Ala Ile Leu Ile Thr Gly Gly Ser Gly
        6988              1365                1370                1375
        6990 Thr Leu Ala Gly Ile Leu Ala Arg His Leu Asn His Pro His Thr Tyr
        6991              1380                1385                1390
        6993 Leu Leu Ser Arg Thr Pro Pro Pro Thr Thr Pro Gly Thr His Ile
        6994           1395                1400                1405
        6996 Pro Cys Asp Leu Thr Asp Pro Thr Gln Ile Thr Gln Ala Leu Thr His
        6997   1410                1415                1420
        6999 Ile Pro Gln Pro Leu Thr Gly Ile Phe His Thr Ala Ala Thr Leu Asp
E--> 7000 425                1430                1435                144
        7002 Asp Ala Thr Leu Thr Asn Leu Thr Pro Gln His Leu Thr Thr Thr Leu
        7003              1445                1450                1455
        7005 Gln Pro Lys Ala Asp Ala Ala Trp His Leu His His His Thr Gln Asn
        7006              1460                1465                1470
        7008 Gln Pro Leu Thr His Phe Val Leu Tyr Ser Ser Ala Ala Ala Thr Leu
        7009           1475                1480                1485
        7011 Gly Ser Pro Gly Gln Ala Asn Tyr Ala Ala Ala Asn Ala Phe Leu Asp
        7012   1490                1495                1500
        7014 Ala Leu Ala Thr His Arg His Thr Gln Gly Gln Pro Ala Thr Thr Ile
E--> 7015 505                1510                1515                152
        7017 Ala Trp Gly Met Trp His Thr Thr Thr Thr Leu Thr Ser Gln Leu Thr
        7018              1525                1530                1535
        7020 Asp Ser Asp Arg Asp Arg Ile Arg Arg Gly Gly Phe Leu Pro Ile Ser
        7021           1540                1545                1550
        7023 Asp Asp Glu Gly Met
        7024           1555
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/940,316

DATE: 11/20/2002
TIME: 11:24:11

Input Set : D:\30062-20026.txt
Output Set: N:\CRF4\11192002\I940316.raw

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7442 <210> SEQ ID NO: 29
7443 <211> LENGTH: 1588
7444 <212> TYPE: PRT
7445 <213> ORGANISM: Artificial Sequence
7447 <220> FEATURE:
7448 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
7449       synthase fragment
7451 <400> SEQUENCE: 29
7452 Met Arg Leu Tyr Glu Ala Ala Arg Arg Thr Gly Ser Pro Val Val Val
7453   1               5                  10                  15
7455 Ala Ala Ala Leu Asp Asp Ala Pro Asp Val Pro Leu Leu Arg Gly Leu
7456          20                  25                  30
7458 Arg Arg Thr Thr Val Arg Arg Ala Ala Val Arg Glu Arg Ser Leu Ala
7459          35                  40                  45
7461 Asp Arg Ser Pro Cys Cys Pro Thr Thr Ser Ala Pro Thr Pro Pro Ser
7462       50                  55                  60
7464 Arg Ser Ser Trp Asn Ser Thr Ala Thr Val Leu Gly His Leu Gly Ala
7465   65                  70                  75                  80
7467 Glu Asp Ile Pro Ala Thr Thr Thr Phe Lys Glu Leu Gly Ile Asp Ser
7468               85                  90                  95
7470 Leu Thr Ala Val Gln Leu Arg Asn Ala Leu Thr Thr Ala Thr Gly Val
7471           100                 105                 110
7473 Arg Leu Asn Ala Thr Ala Val Phe Asp Phe Pro Thr Pro Arg Ala Leu
7474           115                 120                 125
7476 Ala Ala Arg Leu Gly Asp Glu Leu Ala Gly Thr Arg Ala Pro Val Ala
7477       130                 135                 140
7479 Ala Arg Thr Ala Ala Thr Ala Ala Ala His Asp Glu Pro Leu Ala Ile
7480 145                 150                 155                 160
7482 Val Gly Met Ala Cys Arg Leu Pro Gly Gly Val Ala Ser Pro Gln Glu
7483               165                 170                 175
7485 Leu Trp Arg Leu Val Ala Ser Gly Thr Asp Ala Ile Thr Glu Phe Pro
7486           180                 185                 190
7488 Ala Asp Arg Gly Trp Asp Val Asp Ala Leu Tyr Asp Pro Asp Pro Asp
7489           195                 200                 205
7491 Ala Ile Gly Lys Thr Phe Val Arg His Gly Gly Phe Leu Asp Gly Ala
7492       210                 215                 220
7494 Thr Gly Phe Asp Ala Ala Phe Phe Gly Ile Ser Pro Arg Glu Ala Leu
7495 225                 230                 235                 240
7497 Ala Met Asp Pro Gln Gln Arg Val Leu Leu Glu Thr Ser Trp Glu Ala
7498               245                 250                 255
7500 Phe Glu Ser Ala Gly Ile Thr Pro Asp Ala Ala Arg Gly Ser Asp Thr
7501           260                 265                 270
7503 Gly Val Phe Ile Gly Ala Phe Ser Tyr Gly Tyr Gly Thr Gly Ala Asp
7504           275                 280                 285
7506 Thr Asn Gly Phe Gly Ala Thr Gly Ser Gln Thr Ser Val Leu Ser Gly
7507       290                 295                 300
7509 Arg Leu Ser Tyr Phe Tyr Gly Leu Glu Gly Pro Ser Val Thr Val Asp
7510 305                 310                 315                 320
7512 Thr Ala Cys Ser Ser Ser Leu Val Ala Leu His Gln Ala Gly Gln Ser
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7587 Val Asp Val Val Gln Pro Ala Ser Trp Ala Met Met Val Ser Leu Ala
7588                 725             730                 735
7590 Ala Val Trp Gln Ala Ala Gly Val Arg Pro Asp Ala Val Ile Gly His
7591             740             745                 750
7593 Ser Gln Gly Glu Ile Ala Ala Ala Cys Val Ala Gly Ala Val Ser Leu
7594         755             760             765
7596 Arg Asp Ala Ala Arg Ile Val Thr Leu Arg Ser Gln Ala Ile Ala Arg
7597     770             775                 780
7599 Gly Leu Ala Gly Arg Gly Ala Met Ala Ser Val Ala Leu Pro Ala Gln
7600 785             790             795                 800
7602 Asp Val Glu Leu Val Asp Gly Ala Trp Ile Ala Ala His Asn Gly Pro
7603             805             810             815
7605 Ala Ser Thr Val Ile Ala Gly Thr Pro Glu Ala Val Asp His Val Leu
7606         820             825             830
7608 Thr Ala His Glu Ala Gln Gly Val Arg Val Arg Arg Ile Thr Val Asp
7609         835             840             845
7611 Tyr Ala Ser His Thr Pro His Val Glu Leu Ile Arg Asp Glu Leu Leu
7612     850             855             860
7614 Asp Ile Thr Ser Asp Ser Ser Ser Gln Thr Pro Leu Val Pro Trp Leu
7615 865             870             875             880
7617 Ser Thr Val Asp Gly Thr Trp Val Asp Ser Pro Leu Asp Gly Glu Tyr
7618             885             890             895
7620 Trp Tyr Arg Asn Leu Arg Glu Pro Val Gly Phe His Pro Ala Val Ser
7621         900             905             910
7623 Gln Leu Gln Ala Gln Gly Asp Thr Val Phe Val Glu Val Ser Ala Ser
7624         915             920             925
7626 Pro Val Leu Leu Gln Ala Met Asp Asp Val Val Thr Val Ala Thr
7627     930             935             940
7629 Leu Arg Arg Asp Asp Gly Asp Ala Thr Arg Met Leu Thr Ala Leu Ala
7630 945             950             955             960
7632 Gln Ala Tyr Val His Gly Val Thr Val Asp Trp Pro Ala Ile Leu Gly
7633             965             970             975
7635 Thr Thr Thr Thr Arg Val Leu Asp Leu Pro Thr Tyr Ala Phe Gln His
7636             980             985             990
7638 Gln Arg Tyr Trp Leu Glu Ser Ala Pro Pro Ala Thr Ala Asp Ser Gly
7639     995             1000            1005
7641 His Pro Val Leu Gly Thr Gly Val Ala Val Ala Gly Ser Pro Gly Arg
7642     1010            1015            1020
7644 Val Phe Thr Gly Pro Val Pro Ala Gly Ala Asp Arg Ala Val Phe Ile
E--> 7645 025            1030            1035            104
7647 Ala Glu Leu Ala Leu Ala Ala Ala Asp Ala Thr Asp Cys Ala Thr Val
7648             1045            1050            1055
7650 Glu Gln Leu Asp Val Thr Ser Val Pro Gly Gly Ser Ala Arg Gly Arg
7651         1060            1065            1070
7653 Ala Thr Ala Gln Thr Trp Val Asp Glu Pro Ala Ala Asp Gly Arg Arg
7654         1075            1080            1085
7656 Arg Phe Thr Val His Thr Arg Val Gly Asp Ala Pro Trp Thr Leu His
7657     1090            1095            1100
7659 Ala Glu Gly Val Leu Arg Pro Gly Arg Val Pro Gln Pro Glu Ala Val
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E--> 7660 105               1110            1115              112
     7662 Asp Thr Ala Trp Pro Pro Pro Gly Ala Val Pro Ala Asp Gly Leu Pro
     7663            1125            1130            1135
     7665 Gly Ala Trp Arg Arg Ala Asp Gln Val Phe Val Glu Ala Glu Val Asp
     7666       1140          1145          1150
     7668 Ser Pro Asp Gly Phe Val Ala His Pro Asp Leu Leu Asp Ala Val Phe
     7669      1155           1160            1165
     7671 Ser Ala Val Gly Asp Gly Ser Arg Gln Pro Thr Gly Trp Arg Asp Leu
     7672   1170          1175            1180
     7674 Ala Val His Ala Ser Asp Ala Thr Val Leu Arg Ala Cys Leu Thr Arg
E--> 7675 185               1190           1195              120
     7677 Arg Asp Ser Gly Val Val Glu Leu Ala Ala Phe Asp Gly Ala Gly Met
     7678            1205            1210            1215
     7680 Pro Val Leu Thr Ala Glu Ser Val Thr Leu Gly Glu Val Ala Ser Ala
     7681         1220          1225            1230
     7683 Gly Gly Ser Asp Glu Ser Asp Gly Leu Leu Arg Leu Glu Trp Leu Pro
     7684      1235           1240            1245
     7686 Val Ala Glu Ala His Tyr Asp Gly Ala Asp Glu Leu Pro Glu Gly Tyr
     7687   1250           1255            1260
     7689 Thr Leu Ile Thr Ala Thr His Pro Asp Asp Pro Asp Asp Pro Thr Asn
E--> 7690 265               1270           1275              128
     7692 Pro His Asn Thr Pro Thr Arg Thr His Thr Gln Thr Thr Arg Val Leu
     7693            1285            1290            1295
     7695 Thr Ala Leu Gln His His Leu Ile Thr Thr Asn His Thr Leu Ile Val
     7696         1300            1305            1310
     7698 His Thr Thr Thr Asp Pro Pro Gly Ala Ala Val Thr Gly Leu Thr Arg
     7699      1315           1320            1325
     7701 Thr Ala Gln Asn Glu His Pro Gly Arg Ile His Leu Ile Glu Thr His
     7702   1330           1335            1340
     7704 His Pro His Thr Pro Leu Pro Leu Thr Gln Leu Thr Thr Leu His Gln
E--> 7705 345               1350           1355              136
     7707 Pro His Leu Arg Leu Thr Asn Asn Thr Leu His Thr Pro His Leu Thr
     7708            1365            1370            1375
     7710 Pro Ile Thr Thr His His Asn Thr Thr Thr Thr Thr Pro Asn Thr Pro
     7711         1380            1385            1390
     7713 Pro Leu Asn Pro Asn His Ala Ile Leu Ile Thr Gly Gly Ser Gly Thr
     7714      1395           1400            1405
     7716 Leu Ala Gly Ile Leu Ala Arg His Leu Asn His Pro His Thr Tyr Leu
     7717   1410           1415            1420
     7719 Leu Ser Arg Thr Pro Pro Pro Pro Thr Thr Pro Gly Thr His Ile Pro
E--> 7720 425               1430           1435              144
     7722 Cys Asp Leu Thr Asp Pro Thr Gln Ile Thr Gln Ala Leu Thr His Ile
     7723            1445            1450            1455
     7725 Pro Gln Pro Leu Thr Gly Ile Phe His Thr Ala Ala Thr Leu Asp Asp
     7726         1460            1465            1470
     7728 Ala Thr Leu Thr Asn Leu Thr Pro Gln His Leu Thr Thr Thr Leu Gln
     7729      1475           1480            1485
     7731 Pro Lys Ala Asp Ala Ala Trp His Leu His His His Thr Gln Asn Gln
     7732   1490            1495            1500
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Input Set : D:\30062-20026.txt
Output Set: N:\CRF4\11192002\I940316.raw

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       7734 Pro Leu Thr His Phe Val Leu Tyr Ser Ser Ala Ala Ala Thr Leu Gly
E--> 7735 505              1510              1515                  152
       7737 Ser Pro Gly Gln Ala Asn Tyr Ala Ala Ala Asn Ala Phe Leu Asp Ala
       7738               1525              1530              1535
       7740 Leu Ala Thr His Arg His Thr Gln Gly Gln Pro Ala Thr Thr Ile Ala
       7741           1540              1545              1550
       7743 Trp Gly Met Trp His Thr Thr Thr Thr Leu Thr Ser Gln Leu Thr Asp
       7744        1555              1560              1565
       7746 Ser Asp Arg Asp Arg Ile Arg Arg Gly Gly Phe Leu Pro Ile Ser Asp
       7747    1570              1575              1580
       7749 Asp Glu Gly Met
E--> 7750 585
       8164 <210> SEQ ID NO: 31
       8165 <211> LENGTH: 1578
       8166 <212> TYPE: PRT
       8167 <213> ORGANISM: Artificial Sequence
       8169 <220> FEATURE:
       8170 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
       8171        synthase fragment
       8173 <400> SEQUENCE: 31
       8174 Met Arg Leu Tyr Glu Ala Ala Arg Arg Thr Gly Ser Pro Val Val Val
       8175   1           5               10                  15
       8177 Ala Ala Ala Leu Asp Asp Ala Pro Asp Val Pro Leu Leu Arg Gly Leu
       8178               20              25              30
       8180 Arg Arg Thr Thr Val Arg Arg Ala Ala Val Arg Glu Arg Ser Leu Ala
       8181         35              40              45
       8183 Asp Arg Ser Pro Cys Cys Pro Thr Thr Ser Ala Pro Thr Pro Pro Ser
       8184      50              55              60
       8186 Arg Ser Ser Trp Asn Ser Thr Ala Thr Val Leu Gly His Leu Gly Ala
       8187 65              70              75                  80
       8189 Glu Asp Ile Pro Ala Thr Thr Thr Phe Lys Glu Leu Gly Ile Asp Ser
       8190               85              90                  95
       8192 Leu Thr Ala Val Gln Leu Arg Asn Ala Leu Thr Thr Ala Thr Gly Val
       8193               100             105             110
       8195 Arg Leu Asn Ala Thr Ala Val Phe Asp Phe Pro Thr Pro Arg Ala Leu
       8196           115             120             125
       8198 Ala Ala Arg Leu Gly Asp Glu Leu Ala Gly Thr Arg Ala Pro Val Ala
       8199      130             135             140
       8201 Ala Arg Thr Ala Ala Thr Ala Ala Ala His Asp Glu Pro Leu Ala Ile
       8202 145             150             155             160
       8204 Val Gly Met Ala Cys Arg Leu Pro Gly Gly Val Ala Ser Pro Gln Glu
       8205               165             170             175
       8207 Leu Trp Arg Leu Val Ala Ser Gly Thr Asp Ala Ile Thr Glu Phe Pro
       8208           180             185             190
       8210 Ala Asp Arg Gly Trp Asp Val Asp Ala Leu Tyr Asp Pro Asp Pro Asp
       8211      195             200             205
       8213 Ala Ile Gly Lys Thr Phe Val Arg His Gly Gly Phe Leu Asp Gly Ala
       8214      210             215             220
       8216 Thr Gly Phe Asp Ala Ala Phe Phe Gly Ile Ser Pro Arg Glu Ala Leu
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    8364    1010                1015                  1020
    8366 Asp Arg Ala Val Phe Ile Ala Glu Leu Ala Leu Ala Ala Ala Asp Ala
E--> 8367 025                1030              1035              104
    8369 Thr Asp Cys Ala Thr Val Glu Gln Leu Asp Val Thr Ser Val Pro Gly
    8370              1045          .      1050    .        1055
    8372 Gly Ser Ala Arg Gly Arg Ala Thr Ala Gln Thr Trp Val Asp Glu Pro
    8373          1060              1065              1070
    8375 Ala Ala Asp Gly Arg Arg Arg Phe Thr Val His Thr Arg Val Gly Asp
    8376      1075              1080              1085
    8378 Ala Pro Trp Thr Leu His Ala Glu Gly Val Leu Arg Pro Gly Arg Val
    8379    1090              1095              1100        .
    8381 Pro Gln Pro Glu Ala Val Asp Thr Ala Trp Pro Pro Pro Gly Ala Val
E--> 8382 105              1110              1115    .            112
    8384 Pro Ala Asp Gly Leu Pro Gly Ala Trp Arg Arg Ala Asp Gln Val Phe
    8385          1125              1130              1135 .
    8387 Val Glu Ala Glu Val Asp Ser Pro Asp Gly Phe Val Ala His Pro Asp
    8388          1140              1145              1150
    8390 Leu Leu Asp Ala Val Phe Ser Ala Val Gly Asp Gly Ser Arg Gln Pro
    8391          1155              1160      .      .  1165
    8393 Thr Gly Trp Arg Asp Leu Ala Val His Ala Ser Asp Ala Thr Val Leu
    8394     .1170              1175              1180
    8396 Arg Ala Cys Leu Thr Arg Arg Asp Ser Gly Val Val Glu Leu Ala Ala
E--> 8397 185              1190              1195    .    .        120
    8399 Phe Asp Gly Ala Gly Met Pro Val Leu Thr Ala Glu Ser Val Thr Leu
    8400              1205              1210              1215
    8402 Gly Glu Val Ala Ser Ala Gly Gly Ser Asp Glu Ser Asp Gly Leu Leu
    8403          1220              1225          -  --  1230
    8405 Arg Leu Glu Trp Leu Pro Val Ala Glu Ala His Tyr Asp Gly Ala Asp
    8406      1235              1240              1245  -.
    8408 Glu Leu Pro Glu Gly Tyr Thr Leu Ile Thr Ala Thr His Pro Asp Asp
    8409    1250              1255              1260    .
    8411 Pro Asp Asp Pro Thr Asn Pro His Asn Thr Pro Thr Arg Thr His Thr
E--> 8412 265              1270      .          1275              128
    8414 Gln Thr Thr Arg Val Leu Thr Ala Leu Gln His His Leu Ile Thr Thr
    8415              1285              1290              1295   .
    8417 Asn His Thr Leu Ile Val His Thr Thr Thr Asp Pro Pro Gly Ala Ala
    8418          1300              1305              1310
    8420 Val Thr Gly Leu Thr Arg Thr Ala Gln Asn Glu His Pro Gly Arg Ile
    8421 .        1315              1320          .  1325    .
    8423 His Leu Ile Glu Thr His His Pro His Thr Pro Leu Pro Leu Thr Gln
    8424    1330              1335              1340
    8426 Leu Thr Thr Leu His Gln Pro His Leu Arg Leu Thr Asn Asn Thr Leu
E--> 8427 345              1350              1355              136
    8429 His Thr Pro His Leu Thr Pro Ile Thr Thr His His Asn Thr Thr Thr
    8430              1365              1370  .          1375
    8432 Thr Thr Pro Asn Thr Pro Pro Leu Asn Pro Asn His Ala Ile Leu Ile
    8433          1380              1385              1390
    8435 Thr Gly Gly Ser Gly Thr Leu Ala Gly Ile Leu Ala Arg His Leu Asn
    8436          1395              1400              1405   .
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        8438 His Pro His Thr Tyr Leu Leu Ser Arg Thr Pro Pro Pro Thr Thr
        8439     1410              1415              1420
        8441 Pro Gly Thr His Ile Pro Cys Asp Leu Thr Asp Pro Thr Gln Ile Thr
E--> 8442 425              1430              1435                      144
        8444 Gln Ala Leu Thr His Ile Pro Gln Pro Leu Thr Gly Ile Phe His Thr
        8445              1445              1450              1455
        8447 Ala Ala Thr Leu Asp Asp Ala Thr Leu Thr Asn Leu Thr Pro Gln His
        8448              1460              1465              1470
        8450 Leu Thr Thr Thr Leu Gln Pro Lys Ala Asp Ala Ala Trp His Leu His
        8451     1475              1480              1485
        8453 His His Thr Gln Asn Gln Pro Leu Thr His Phe Val Leu Tyr Ser Ser
        8454     1490              1495              1500
        8456 Ala Ala Ala Thr Leu Gly Ser Pro Gly Gln Ala Asn Tyr Ala Ala Ala
E--> 8457 505              1510              1515                      152
        8459 Asn Ala Phe Leu Asp Ala Leu Ala Thr His Arg His Thr Gln Gly Gln
        8460              1525              1530              1535
        8462 Pro Ala Thr Thr Ile Ala Trp Gly Met Trp His Thr Thr Thr Thr Leu
        8463              1540              1545              1550
        8465 Thr Ser Gln Leu Thr Asp Ser Asp Arg Asp Arg Ile Arg Arg Gly Gly
        8466     1555              1560              1565
        8468 Phe Leu Pro Ile Ser Asp Asp Glu Gly Met
        8469     1570              1575
        8891 <210> SEQ ID NO: 33
        8892 <211> LENGTH: 1605
        8893 <212> TYPE: PRT
        8894 <213> ORGANISM: Artificial Sequence
        8896 <220> FEATURE:
        8897 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic PKS
        8898       synthase fragment
        8900 <400> SEQUENCE: 33
        8901 Met Arg Leu Tyr Glu Ala Ala Arg Arg Thr Gly Ser Pro Val Val Val
        8902   1               5                  10                  15
        8904 Ala Ala Ala Leu Asp Asp Ala Pro Asp Val Pro Leu Leu Arg Gly Leu
        8905              20                  25                  30
        8907 Arg Arg Thr Thr Val Arg Arg Ala Ala Val Arg Glu Arg Ser Leu Ala
        8908              35                  40                  45
        8910 Asp Arg Ser Pro Cys Cys Pro Thr Thr Ser Ala Pro Thr Pro Pro Ser
        8911     50                  55                  60
        8913 Arg Ser Ser Trp Asn Ser Thr Ala Thr Val Leu Gly His Leu Gly Ala
        8914   65                  70                  75                  80
        8916 Glu Asp Ile Pro Ala Thr Thr Thr Phe Lys Glu Leu Gly Ile Asp Ser
        8917              85                  90                  95
        8919 Leu Thr Ala Val Gln Leu Arg Asn Ala Leu Thr Thr Ala Thr Gly Val
        8920              100                 105                 110
        8922 Arg Leu Asn Ala Thr Ala Val Phe Asp Phe Pro Thr Pro Arg Ala Leu
        8923              115                 120                 125
        8925 Ala Ala Arg Leu Gly Asp Glu Leu Ala Gly Thr Arg Ala Pro Val Ala
        8926     130                 135                 140
        8928 Ala Arg Thr Ala Ala Thr Ala Ala Ala His Asp Glu Pro Leu Ala Ile
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9076      930                 935                 940
9078 Ser Pro Val Leu Leu Gln Ala Met Asp Asp Asp Val Val Thr Val Ala
9079 945                 950                 955                 960
9081 Thr Leu Arg Arg Asp Asp Gly Asp Ala Thr Arg Met Leu Thr Ala Leu
9082                965                 970                 975
9084 Ala Gln Ala Tyr Val His Gly Val Thr Val Asp Trp Pro Ala Ile Leu
9085          980                 985                 990
9087 Gly Thr Thr Thr Thr Arg Val Leu Asp Leu Pro Thr Tyr Ala Phe Gln
9088         995                1000                1005
9090 His Gln Arg Tyr Trp Leu Glu Ser Ala Pro Pro Ala Thr Ala Asp Ser
9091    1010                1015                1020
9093 Gly His Pro Val Leu Gly Thr Gly Val Ala Val Ala Gly Ser Pro Gly
E--> 9094 025                1030                1035                104
9096 Arg Val Phe Thr Gly Pro Val Pro Ala Gly Ala Asp Arg Ala Val Phe
9097                1045                1050                1055
9099 Ile Ala Glu Leu Ala Leu Ala Ala Ala Asp Ala Thr Asp Cys Ala Thr
9100          1060                1065                1070
9102 Val Glu Gln Leu Asp Val Thr Ser Val Pro Gly Gly Ser Ala Arg Gly
9103    1075                1080                1085
9105 Arg Ala Thr Ala Gln Thr Trp Val Asp Glu Pro Ala Ala Asp Gly Arg
9106    1090                1095                1100
9108 Arg Arg Phe Thr Val His Thr Arg Val Gly Asp Ala Pro Trp Thr Leu
E--> 9109 105                1110                1115                112
9111 His Ala Glu Gly Val Leu Arg Pro Gly Arg Val Pro Gln Pro Glu Ala
9112                1125                1130                1135
9114 Val Asp Thr Ala Trp Pro Pro Pro Gly Ala Val Pro Ala Asp Gly Leu
9115          1140                1145                1150
9117 Pro Gly Ala Trp Arg Arg Ala Asp Gln Val Phe Val Glu Ala Glu Val
9118    1155                1160                1165
9120 Asp Ser Pro Asp Gly Phe Val Ala His Pro Asp Leu Leu Asp Ala Val
9121    1170                1175                1180
9123 Phe Ser Ala Val Gly Asp Gly Ser Arg Gln Pro Thr Gly Trp Arg Asp
E--> 9124 185                1190                1195                120
9126 Leu Ala Val His Ala Ser Asp Ala Thr Val Leu Arg Ala Cys Leu Thr
9127          1205                1210                1215
9129 Arg Arg Asp Ser Gly Val Val Glu Leu Ala Ala Phe Asp Gly Ala Gly
9130          1220                1225                1230
9132 Met Pro Val Leu Thr Ala Glu Ser Val Thr Leu Gly Glu Val Ala Ser
9133    1235                1240                1245
9135 Ala Gly Gly Ser Asp Glu Ser Asp Gly Leu Leu Arg Leu Glu Trp Leu
9136    1250                1255                1260
9138 Pro Val Ala Glu Ala His Tyr Asp Gly Ala Asp Glu Leu Pro Glu Gly
E--> 9139 265                1270                1275                128
9141 Tyr Thr Leu Ile Thr Ala Thr His Pro Asp Asp Pro Asp Asp Pro Thr
9142          1285                1290                1295
9144 Asn Pro His Asn Thr Pro Thr Arg Thr His Thr Gln Thr Thr Arg Val
9145          1300                1305                1310
9147 Leu Thr Ala Leu Gln His His Leu Ile Thr Thr Asn His Thr Leu Ile
9148    1315                1320                1325
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     9150 Val His Thr Thr Thr Asp Pro Pro Gly Ala Ala Val Thr Gly Leu Thr
     9151    1330              1335              1340
     9153 Arg Thr Ala Gln Asn Glu His Pro Gly Arg Ile His Leu Ile Glu Thr
E--> 9154 345               1350              1355                136
     9156 His His Pro His Thr Pro Leu Pro Leu Thr Gln Leu Thr Thr Leu His
     9157                1365              1370              1375
     9159 Gln Pro His Leu Arg Leu Thr Asn Asn Thr Leu His Thr Pro His Leu
     9160           1380         .        1385              1390
     9162 Thr Pro Ile Thr Thr His His Asn Thr Thr Thr Thr Thr Pro Asn Thr
     9163        1395              1400              1405
     9165 Pro Pro Leu Asn Pro Asn His Ala Ile Leu Ile Thr Gly Gly Ser Gly
     9166    1410              1415              1420
     9168 Thr Leu Ala Gly Ile Leu Ala Arg His Leu Asn His Pro His Thr Tyr
E--> 9169 425               1430              1435                144
     9171 Leu Leu Ser Arg Thr Pro Pro Pro Thr Thr Pro Gly Thr His Ile
     9172           .    1445              1450              1455
     9174 Pro Cys Asp Leu Thr Asp Pro Thr Gln Ile Thr Gln Ala Leu Thr His
     9175           1460              1465       ...    1470
     9177 Ile Pro Gln Pro Leu Thr Gly Ile Phe His Thr Ala Ala Thr Leu Asp
     9178        1475    .         1480         .    1485
     9180 Asp Ala Thr Leu Thr Asn Leu Thr Pro Gln His Leu Thr Thr Thr Leu
     9181    1490              1495              1500
     9183 Gln Pro Lys Ala Asp Ala Ala Trp His Leu His His His Thr Gln Asn
E--> 9184 505               1510              1515                152
     9186 Gln Pro Leu Thr His Phe Val Leu Tyr Ser Ser Ala Ala Ala Thr Leu
     9187                1525              1530              1535
     9189 Gly Ser Pro Gly Gln Ala Asn Tyr Ala Ala Ala Asn Ala Phe Leu Asp
     9190           1540              1545              1550
     9192 Ala Leu Ala Thr His Arg His Thr Gln Gly Gln Pro Ala Thr Thr Ile
     9193        1555              1560              1565
     9195 Ala Trp Gly Met Trp His Thr Thr Thr Thr Leu Thr Ser Gln Leu Thr
     9196    1570              1575              1580
     9198 Asp Ser Asp Arg Asp Arg Ile Arg Arg Gly Gly Phe Leu Pro Ile Ser
E--> 9199 585               1590              1595                160
     9201 Asp Asp Glu Gly Met
     9202                1605
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VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/940,316**

DATE: 11/20/2002
TIME: 11:24:13

Input Set : **D:\30062-20026.txt**
Output Set: **N:\CRF4\11192002\I940316.raw**

L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:2519 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:3448 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
M:332 Repeated in SeqNo=17
L:4135 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:19
M:332 Repeated in SeqNo=19
L:4818 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:21
M:332 Repeated in SeqNo=21
L:5503 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:23
M:332 Repeated in SeqNo=23
L:6210 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:25
M:332 Repeated in SeqNo=25
L:6925 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:27
M:332 Repeated in SeqNo=27
L:7645 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:29
M:332 Repeated in SeqNo=29
L:8367 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:31
M:332 Repeated in SeqNo=31
L:9094 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:33
M:332 Repeated in SeqNo=33